

FIG. 1A

Sequence I

-72 AGGAAACCTGCC

-60 ATGGCCTCCTGGTGAGCTGTCTCCTCATCCACTGCTCGCTGCCTCTCCAGATACTCTGACCC

1 M D P L G A A K P Q W P R R C L A A L

1 ATGGATCCCCCTGGGTGCAGCCAAGCCACAATGGCCATGGCGCGCTGTCTGGCCGCACTG

21 L F Q L L V A V C F F S Y L R V S R D D

61 CTATTTCAGCTGCTGGTGGCTGTGTGTTCTTCTCTCTACCTGCGTGTGTCTCCGAGACGAT

41 A T G S P R A P S G S S R Q D T T P T R

121 GCCACTGGATCCCCCTAGGCTCCCAAGTGGTCCCTCCGACAGGACACCACTCCCAACCCGC

61 P T L L I L L W T W P F H I P V A L S R

181 CCCACCCTCCTGATCCTGTCTATGGACATGGCCTTCCACATCCCTGTGGCTCTGTCCCGC

81 C S E M V P G T A D C H I T A D R K V Y

241 TGTTCAGAGATGGTGCCCGGCACAGCCGACTGCCACATCACTGCCGACCCGAAGGTGTAC

101 P Q A D T V I V H H W D I M S N P K S R

301 CCACAGGCAGACACGGTCACTCGTGCACTGGGATATCATGTCCAACCTTAAGTCACGC

121 L P P S P R P Q G Q R W I W F N L E P P

361 CTCCCACCTTCCCCGAGGCCCGCAGGGCAGCGCTGGATCTGGTTCAACTGGAGCCACCC

141 P N C Q H L E A L D R Y F N L T M S Y R

421 CCTAACTGCCAGCACCTGGAAGCCCTGGACAGATACTTCAATCTCACCATGTCTTACCCG

161 S D S D I F T P Y G W L E P W S G Q P A

481 AGGACTCCGACATCTTACGCCCTACGGCTGGCTGGAGCCGTGGTCCGGCCAGCCTGCCA

181 H P P L N L S A K T E L V A W A V S N W

541 CACCCACCGCTCAACCTCTCGGCCAAGACCGAGCTGTGTGGCTGGCGGTGTCCAACCTGG

FIG. 1B

201 K P D S A R V R Y Y Q S L Q A H L K V D
 601 AAGCGGACTCAGCCAGGTGCGCTACTACAGAGCCTGCAGGCTCATCTCAAGTGGAC

221 V Y G R S H K P L P K G T M M E T L S R
 661 GTGTACGGACGCTCCACAAGCCCTGCCCAAGGGACCATGATGGAGACGCTGTCCCGG

241 Y K F Y L A F E N S L H P D Y I T E K L
 721 TACAAGTTCTACCTGGCCTTCGAGAACTCCTTGACCCCGACTACATCACCAGAGAAGCTG

261 W R N A L E A W A V P V L G P S R S N
 781 TGGAGGAACGCCCTGGAGGCTGCCCGTGCCCGTGGTGCTGGGCCCCAGCAGAAAGCAAC

281 Y E R F L P P D A F I H V D D F Q S P K
 841 TACGAGAGGTTCCCTGCCACCCGACGCTTCATCCACGTGGACGACTTCCAGAGCCCCAAG

301 D L A R Y L Q E L D K D H A R Y L S Y F
 901 GACCTGGCCCGGTACCTGCAGGAGCTGGACAGGACCAAGCCCGCTACCTGAGCTACTTT

321 R W R E T L R P R S F S W A L D F C K A
 961 CGCTGGCGGAGACGCTGGGCCCTCGCTCCTTCAAGTGGCACTGGATTCTGCAAGGCC

341 C W K L Q Q E S R Y Q T V R S I A A W F
 1021 TGCTGGAACTGCAGCAGGAATCCAGGTACAGACGCTGCGCAGCATAGCGGCTTGTTTC

361 T *
 1081 ACCTGAGAGCCGGCATGGTGCCCTGGGCTGCCGGGAACCTCATCTGCCCTGGGGCCTCACC

1141 TGCTGGAGTCCTTTGTGGCCAAACCTCTCTCTTACTTGGGACCTCACACGCTGGGCTTCA

1201 CGGCTGCCAGGAGCCTCTCCCCCTCCAGAAGACTTGCTGCTAGGGACCTCGCCTGCTGGG

1261 GACCTCGCCTGTGGGACCTCACCTGCTGGGACCTCACCTGCTGGGACCTTGCTGGCTGC

1321 TGGAGGCTGCACCTACTGAGGATGTGGGGGTGGGGGACTTTACCTGCTGGGACCTGCTC
 1381 CCAGAGACCTTGCCACACTGAATCTCACCTGCTGGGGACCTCACCCCTGGAGGGCCCTGGG
 1441 CCCTGGGGAACCTGGCTTACTTGGGGCCCCACCCGGGAGTGATGGTCTGGCTGATTGTT
 1501 TGTGATGTTGTAGCCGCCCTGTGAGGGGTGCAGAGAGATCATCACGGCACGGTTTCCAGA
 1561 TGTAATACTGCAAGGAAAAATGATGACGTGTCTCCTCACTCTAGAGGGGTGGTCCCCTG
 1621 GGTTAAGAGCTCACCCACAGGTCTCACCTCAGGGGTTAAGAGCTCAGAGTTCAGACAGGT
 1681 CCAAGTTCAGCCAGGACCACCACTTATAGGGTACAGGTGGGATCGACTGTAAATGAGG
 1741 ACTTCTGGAACATTCCAAATATTCTGGGGTTGAGGGGAAATTGCTGCTGTCTACAAAATGC
 1801 CAAGGGTGGACAGGCGCTGTGGCTCACGCCCTGTAATTCACGACACTTTGGGAGGCTGAGGT
 1861 AGGAGGATTGATTGAGGCCAACAGTTAAAGACCAGCCTGGTCAATATAGCAAGACCACGT
 1921 CTCTAAATAAAAAATAATAGGCCGGCCAGGAAAAAATAAAAAAATAAAAAA

FIG. 1C

FIG. 2A

Sequence II

-276 CCTTCCCTTGCTAGACTCTTCTTGGAATGAGAAAGTAC

-240 CGATTCTGCTGAAGACCTCGCGCTCTCAGGCTCTGGAGTTGGAACCCCTGTACCTTCCTT

-180 TCCTCTGCTGAGCCCTGCCTCCTTAGGAGCCAGAGCTCGACAGAACTCGGTTGCTTTG

-120 CTGTTTGCTTTGGAGGGAACACAGCTGACGATGAGGCTGACTTTGAACTCAAGAGATCTG

-60 CTTACCCAGTCTCCTGGAATTAAGGCTGTACTACATTTGCTGGACCTAAGATTTTC

1 M I T M L Q D L H V N K I S M S R S K S

1 ATGATCACTATGCTTCAAGATCTCCATGTCAACAAGATCTCCATGTCAAGATCCAAGTCA

21 E T S L P S S R S G S Q E K I M N V K G

61 GAAACAAGTCTTCCATCCTCAAGATCTGGATCACAGGAGAAAATAATGATGTCAAGGGA

41 K V I L L M L I V S T V V V V F W E Y V

121 AAAGTAATCCTGTTGATGCTGATTGTCTCAACCGTGGTTGCTGTTTGGGAATATGTC

61 N R I P E V G E N R W Q K D W W F P S W

181 AACAGAATCCAGAGGTTGGTGAGAACAGATGGCAGAGGACTGGTGGTTCCCAAGCTGG

81 F K N G T H S Y Q E D N V E G R R E K G

241 TTATAAATGGGACCCACAGTTATCAAGAAGACACAGTAGAGGACGGAGAGAAAAGGTT

101 R N G D R I E E P Q L W D W F N P K N R

301 AGAAATGGAGATCGCATTTGAAGAGCCTCAGCTATGGGACTGTTCAATCCAAAGAACCGC

121 P D V L T V T P W K A P I V W E G T Y D

361 CCGGATGTTTGTGACAGTGACCCCGTGGAGGCGCGGATTTGTGTGGAGGCACTTATGAC

FIG. 2B

141	T A L L E K Y Y A T Q K L T V G L T V F
421	ACAGCTCTGCTGGAAGTACTAGCCACACAGAACTCACTGTGGGCTGACAGTGTTT
161	A V G K Y I E H Y L E D F L E S A D M U
481	GCTGTGGAAAGTACATTGAGCATTAAGAGACTTTCTGGAGTCTGCTGACATGTAC
181	F M V G H R V I F Y V M I D D T S R M P
541	TTTCATGGTTGGCCATCGGGTCATATTTACGTCATGATAGACGACACCTCCCGGATGCCT
201	V V H L N P L H S L Q V F E I R S E K R
601	GTCGTGCACCTGAACCTCTACATTCCTTACAAGTCTTTGAGATCAGGCTCTGAGAAAGAGG
221	W Q D I S M M R M K T I G E H I L A H I
661	TGGCAGGATATCAGCATGATGGCATGAAGACCATTGGGAGCACATCTCTGGCCACATC
241	Q H E V D F L F C M D V D Q V F Q D N F
721	CAGCAGAGGTCGACTTCTCTCTGTCATGGACGTGGATCAAGTCTTTCAAGACAACTTC
261	G V E T L G Q L V A Q L Q A W W Y K A S
781	GGGGTGGAAACTCTGGCCAGCTGGTAGCACAGCTCCAGGCCCTGGTGGTACAAGGCCAGT
281	P E K F T Y E R R E L S A A Y I P F G E
841	CCCGAGAAAGTTCACCTATGAGAGCGGGAAGTGTGGCCGGGTACATTCCTTCGGAGAG
301	G D F Y Y H A A I F G G T P T H I L N L
901	GGGGATTTTACTACCACCGCGCCATTTTGGAGGAACGCTACTCACATTCTCAACCTC
321	T R E C F K G I L Q D K K H D I E A Q W
961	ACCAGGGAGTGCTTTAAGGGGATCCTCCAGGACAAGAAACATGACATAGAAGCCAGTGG
341	H D E S H L N K Y F L F N K P T K I L S
1021	CATGATGAGGCCACCTCAACAAATACTTCTCTTTTCAACAAACCCACTAAATCCTATCT

361	P E Y C W D Y Q I G L P S D I K S V K V
1081	CCAGAGTATTGCTGGGACTATCAGATAGGCCTGCCCTTCAGATATTAAAGTGTC AAGGTA
381	A W Q T K E Y N L V R N N V *
1141	GCTTGGCAGACAAAGAGTATAATTGTTAGAAATAATGTCTGACTTCAA AATTGTGATG
1201	GAAACTTGACACTATTCTTAACCA

FIG. 2C

Sequence III

10	20	30	40	50	60
GAATTCATCGTGGCAAGGCAGCCTGAATGGATGATGTAACTGGGTCTTTCAATGG					
70	80	90	100	110	120
AGGGCCAGACTCCTGGGTCTAGGGGATGAGGAGGGAGGATCGGGTTAGCTGGGACCCA					
130	140	150	160	170	180
GGTGAAAGGGGCTGGGGCCACATTCCTGAGTCTCAGAGAGAAGGATCTGGGTCTCAA					
190	200	210	220	230	240
GCACCTGAGTCGGAGGAGGAGGGGTGCTGGCTCCTGGAAACCACCTCTTGGACCAT					
250	260	270	280	290	300
CTATGCAGATCAGCAGAACCAAGAGAAATTTCTGCGCCCATCTGAATTTCTAAGTTGG					
310	320	330	340	350	360
GGGAGGGCGTGATCTGACACTGAGGTTCTTGTATCCTCAGCAAGCGGCAATTGCTGTA					
370	380	390	400	410	420
TGAAAGAAGCGACCGCATCTGAGACACAAGTATCCTGCCTTGAAGCCTCTCACCTGGCC					
430	440	450	460	470	480
GTGGCCCAACCTCAACCTCATCTGTCCCTGCTCAGATGCTCAGACCCCTGGACATCCCAGC					
490	500	510	520	530	540
CTCCCTCCTGATGCAATCCTGGTGTCTTTTCCACAGAGAAGCCATCCCAGGCCAG					
550	560	570	580	590	600
GCAGGTGCTCCTGAAATAACCTGGGGGAGGGGTGGCTGAAAGTCCCTGACTGGAGTTGG					
610	620	630	640	650	660
CAGCCAAGCCAGGCCCTGGAGTGGGCGCACCAGAGGGAAGACAGGTTGGCTAATTTCTCTGG					

FIG. 3A

FIG. 3B

670	680	690	700	710	720
AGCCCCTAAGGGTGCAAGGGTAGGCCCTTCTGTGCTGAGGGAGGAGGGCTGGGGCTCTGG					
730	740	750	760	770	780
ACTCCTGGGTCTGAGGGAGGAGGGGTGGGGGCCCTGGACTCCTGGGTCTGAGGGAGGAGG					
790	800	810	820	830	840
GTCTGGGCCTGTACTCCTGGATCTGAGGGAGGAGGGCTGGGAACTTGGGCTCCTGGGT					
850	860	870	880	890	900
CTGAGGGAGGAGGAGCTTTGGTCTGGACTCCTGGGTCTGAGGGAGTAGGGCTAGGGAT					
910	920	930	940	950	960
CTGGACTCGTGGGTGTGAGGAAGGAGGGCTGGGTCTGGACTCCTGGGTCTGAGGAAG					
970	980	990	1000	1010	1020
GAGGGGCAGGGGCTTGGACTCCTGGGTCTGAGGAAGGAGGGCCGGAGCCTGGACTCC					
1030	1040	1050	1060	1070	1080
TAAGTCTGAGGGAGGAGGTCTGGGGCCCTGGACTGCTGGGTGTGAGCACAAAGGCTCTGG					
1090	1100	1110	1120	1130	1140
GTGCTGGGAGTCCCAGCCCTGGGAGATGATGGTTAACTTCTGGGAATCAAGTCAAAC					
1150	1160	1170	1180	1190	1200
CCTGAGTCTTTGACATTGATGTATCTTGAATGGAGGCTCAGTCTGTGGGAAGGATTAC					
1210	1220	1230	1240	1250	1260
CCAGGTCCGAGGCAAGAGACTGAAGGCACAACTGTTTCAGTATAATAAGAAAAATAGT					
1270	1280	1290	1300	1310	1320
TAGAATAAGAATAGTTATCATACAAATTAGATATAGAGATGATCATGGACAGTATCAATC					

1330 1340 1350 1360 1370 1380
ATTAGTAAACATTATTAATCATTAGCTATTACTTTTATTCTTTGTTGATAACTAATA
1390 1400 1410 1420 1430 1440
TAACCAGGAAACAACCGGTGGGTATAGGTCAGGTACTGAAGGGACATTGTGAGAAGTGA
1450 1460 1470 1480 1490 1500
CCTAGAAGGCAAGAGGTGAGCCTTCTGTCAACCGGCATAAAGGGCCTCTTGAGGGCTCCT
1510 1520 1530 1540 1550 1560
TGGTCAAGGGGAACGCCAGTGTCTGGGAAGGCACCCGTTACTCAGCAGACCACGAAAGG
1570 1580 1590 1600 1610 1620
GAATCTCCTTTTCTTGGAGGAGTCAGGGAACACTCTGCTCCACCAGCTTCTTGTGGGAGG
1630 1640 1650 1660 1670 1680
CTGGGTATTATCTAGGCCCTGCCCGCAGTCATCCTGCTGTGCTTCAATGGTCACGC
1690 1700 1710 1720 1730 1740
TCCTTGTCCTCTTGCAATTTTCCCTCCCGTACTCCTGGTTCCCTCTTTGAAGTTCGTAGTAGA
1750 1760 1770 1780 1790 1800
TAGCGGTAGAGAAATAGTGAAAGCCTTTTCTTTTGTGAGCGGAGTCTCGCTC
1810 1820 1830 1840 1850 1860
TGTCCTCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAATCTCCGCCCTCCTGG
1870 1880 1890 1900 1910 1920
GTTACACCATTTCTCCTGCCTCACCTCCCAAATAGCTAGGACTACAGGCGCCCTCCACC
1930 1940 1950 1960 1970 1980
ACGCGCCCGGATAATTTTGTATTTTAGTAGAGACAGGGTTTCAACCGTGTAGCCAGG

FIG. 3C

FIG. 3D

1990	2000	2010	2020	2030	2040
ATGGCCTCCACCTCCTGACCTTGATCCGCCCGCTCAGCCTCCCAAAGTCTGGGATT					
2050	2060	2070	2080	2090	2100
ACAGGCGTGAGCCACCGCGCCCGCCGAAATAGTGAAGTCTTAAAGTCTTTGATCTTTC					
2110	2120	2130	2140	2150	2160
TTATAAGTGCAGAGAGAAACCGCTGACATATGCTGCTTCTCTTCTGCTTCGGCTGCC					
2170	2180	2190	2200	2210	2220
TAAAGGGAAGGGCCCCCTGTCCCATGATCACGTGACTTGCTTGACCTTATCAGTCATTT					
2230	2240	2250	2260	2270	2280
GGACGACTCACCTCCTTATCCTGCTGCCCCCTTGCTTGATACAAATAATATCAGCGCG					
2290	2300	2310	2320	2330	2340
CCCAGCCATTGGGGCCACTACCGGTCTCTGCGTCTTGATGTTAGTGGTCCCCCGGGCCC					
2350	2360	2370	2380	2390	2400
AGCTGTTTTCTCTTATCTCTTTGTCTTGCTTTTATTTCTTACAATCTCTCCTCTCCT					
2410	2420	2430	2440	2450	2460
CACAGGGAAGAAACACCCACCCGCAAGCCCGTAGGGCTGGACCTACGTTAGCCTGCC					
2470	2480	2490	2500	2510	2520
CTGCTCGGGTTGGCGATGCTGGAGGTGGGCTTGACCCAGAGAAAATGCTTAAATTAGG					
2530	2540	2550	2560	2570	2580
TGACAAGCGGCGAGAGCCCTTTGTCTCTGGCGCGGACCCACGCGCCCCCGCTGACGGCG					
2590	2600	2610	2620	2630	2640
TGGGAACAGACCCCTGTTCCACTCCGGTCTCCAGCCTTGAATGGTTGCCCTTCGTGCAGT					

FIG. 3E

2650 2660 2670 2680 2690 2700
 GCAGGCTGGAAGTAGCAGTTTGGCAGGGACCCCTAGAAATCCCCAAAGGAGTGACTA
 2710 2720 2730 2740 2750 2760
 GGGGCTGGGATTCTGGAAATTGAGTGTGACGGTGAGCGGGGGGTGTGGGAGATCGGAG
 2770 2780 2790 2800 2810 2820
 ACCCTGTGGCGCGGAGACACCTGCAGGCTGGAGGCCCTCGCGCGCTCCGGCGGACGCC
 2830 2840 2850 2860 2870 2880
 TGGCAAACAGGTTCTCCATCCCCCAGGAGGACCGGGCAGAGGGCGGACGATCGCTCCACT
 2890 2900 2910 2920 2930 2940
 CGCCGGACACAGGTGCGGGGGCCCTGCCAGCCGCTGGGCGTGCCAGGCTCGAAGCAC
 2950 2960 2970 2980 2990 3000
 CCAGGTGTCGGGGCCGACTCTAAGCCCTGGCACCCGGAAGAGAGAGGGCGGGGATTGGA
 3010 3020 3030 3040 3050 3060
 CCTCCCGGCTCCAGCATTGCAACTGGGCGCTCCGTCTCCTGGTCCACGCAATGATGCTGC
 3070 3080 3090 3100 3110 3120
 GGCTGCTCAGAAAGCCAGGTAGCCTGCCCTGGGTGAAGCCCTTCGCGCAGGTCAATGACGGG
 3130 3140 3150 3160 3170 3180
 GCGGAGGGCAGGGCGCGGTCCCCTGTCATCCCCGATCTGGGGAGCGGTGGGCCACGGGC
 3190 3200 3210 3220 3230 3240
 CATCGCCTTAGCCCCCTGGCGCTGGGCTCGGGCCAAAGTACGGGGCGGGCTCCACCTTC
 3250 3260 3270 3280 3290 3300
 CAGCCATCCGCCCGGGGGAGGGCGGACGCTGCGAGACTCCCGCGCGGCCCTCTCCT

3310 3320 3330 3340 3350 3360
 TCCTCTCCTCCCAAGCCCTCGCTGCCAGTCCGGACAGGCTGCGGAGGGAGGGCTGC

3370 3380 3390 3400 3410 3420
 CGGGCCGGATAGCCGGACGCCCTGGCGTTCCAGGGGCGCGGATGTGGCCTGCCCTTTGCG

3430 3440 3450 3460 3470 3480
 GAGGGTGGCTCCGGCCACGAAAAGCGGACTGTGGATCTGCCACCTGCAAGCAGCTCGGC

3490 3500 3510 3520 3530 3540
 TAAGTGGGACTGCCCCACTCACTAGTTGTTCTCTGGGACCCAGGAACAACCTTCAGAACCA

3550 3560 3570 3580 3590 3600
 GGAGGTGACCCCAACCTCTCTCCAGGTCTTCTAAGGCCCTAGGAATCTCCGCCACC

3610 3620 3630 3640 3650 3660
 TCCCCAGCCATTACTCTCCAGGAACCAAGATGCTCCTTCGGCTCCTGACCCCTCCAGCCT

3670 3680 3690 3700 3710 3720
 CTCCTGTTTACTTGAACATATCGTTTCCCATCACCACTCTGTGGTGATTTTGGCCTC

3730 3740 3750 3760 3770 3780
 ACAGACAGGTACTCCTGAGAAACAGGCTGGTGAAGAGTCCAGTATCAGCGGAACCTTASC

3790 3800 3810 3820 3830 3840
 AGGAGGGGAGACTCGAGATTCTCTCAGGAAAGGTGTAGGAACCTGGACCACCTTCTTTT

3850 3860 3870 3880 3890 3900
 TTTTTTTTTTTTTTAAAGACAGGGTCCCTCTCTGTCCGGCAAGCTGGAGTGCAGTCAG

3910 3920 3930 3940 3950 3960
 CGGTGCTATCGGGCTCATTTGTGAGCTCCGGGGATCCTCCCGCCTTAGCATCCGGGTGATAG

FIG. 3F

T0402T 54E3860

FIG. 36

3970 3980 3990 4000 4010 4020
CTGAGACCACAGACATGTGCCACCATGCCAAGCTAATTTATTTATTTTGGAGAC
4030 4040 4050 4060 4070 4080
GGAGTTTCACTCTTGTGCCAGGCTGGAGTGTAATGGCATGATCTCAGCTCACCGCAAC
4090 4100 4110 4120 4130 4140
TCCCGCCCCGGGTTCAGGCGATTCTCTGCCTCAGCCTCCCGAGTGGCTGGGATTACA
4150 4160 4170 4180 4190 4200
GGCATGCGCCACCATGCCCGGCTAATTTGTATTTTAAGTAGAGACAGGTTTCTCCACG
4210 4220 4230 4240 4250 4260
TTGGTCAGGCTGGTCTCGAACTCCCAACCTCAGGTGATCCACCCACCTTGCCCTCCCAA
4270 4280 4290 4300 4310 4320
GTGCTGGGATTACAGGTGTGAGCCACCGCGCTGGCCCATGCCAAGCTAATTTTAAATT
4330 4340 4350 4360 4370 4380
TTTTTGAAGAGTGCTCTGTGGCCAGGCTGATCTTGAACCTCTGGGCTCAAGGGATCCT
4390 4400 4410 4420 4430 4440
CCCATCTCAGCCCTCCCAATATGCTGGGATTACAGGTGTGAGCCACAGTGCCAGCCAAAC
4450 4460 4470 4480 4490 4500
CATGGCTATCTTGAAAACCACTTGCTCTCCAGTCCCCCATGCCCGAAATTCGAAGGCTCT
4510 4520 4530 4540 4550 4560
CATCCCTGAACCTAGGACTCAGGCTCTCCCTACCTCAGCCCCCAGGAGTCTAAACCTTTA
4570 4580 4590 4600 4610 4620
ACTTCCCTCTTTCCCTGGGACTAAGAGGTGCTGCACCCAGGGGCTCCCTTACCCACAT

FIG. 3H

4630	4640	4650	4660	4670	4680
CCCTCCTCAGCCTCCCTCCTCAGCCTCAGTGCAATTCGCTTTCCTCCCTG					
4690	4700	4710	4720	4730	4740
CAGCCATGTGGCTCGGAGCCATCGTCAGCTCTGCCCTTCCTGCTAGTGTGTC					
MetTrpLeuArgSerHisArgGlnLeuCysLeuAlaPheLeuValCysVal					
4750	4760	4770	4780	4790	4800
TCTCTGTAATCTTCTCCTCATAATCCATCAAGACAGCTTTCACATGGCCTAGGCCTGT					
euSerValIlePhePheLeuHisIleHisGlnAspSerPheProHisGlyLeuGlyLeus					
4810	4820	4830	4840	4850	4860
CGATCCTGTGCCAGACCGCGCCTGTGTGACACCCCGAGTGGCCATCTTCTGCCTGCCGG					
erIleLeuCysProAspArgArgLeuValThrProProValAlaIlePheCysLeuProG					
4870	4880	4890	4900	4910	4920
GTA CTGGATGGCCCCAACGCTCCTCTCTCTGTCGCCAGCACCTGCTTCCCTCTCCG					
lyThrAlaMetGlyProAsnAlaSerSerSerCysProGlnHisProAlaSerLeuSerG					
4930	4940	4950	4960	4970	4980
GCACCTGGACTGTCTACCCCAATGGCCGTTTGGTAATCAGATGGGACAGTATGCCACGC					
lyThrTrpThrValTyrrProAsnGlyArgPheGlyAsnGlnMetGlyGlnTyrrAlaThrL					
4990	5000	5010	5020	5030	5040
TGCTGGCTCTGGCCAGCTCAACGGCCGCGGCTTTATCCTGCTGCCATGCATGCCG					
euLeuAlaLeuAlaGlnLeuAsnGlyArgArgAlaPheIleLeuProAlaMetHisAlaA					
5050	5060	5070	5080	5090	5100
CCCTGGCCCCGGTATTCGCGCATCACCCCTGCCCCGTGCTGGCCCCAGAGTGACAGCCGCA					
laLeuAlaProValPheArgIleThrLeuProValLeuAlaProGluValAspSerArgT					
5110	5120	5130	5140	5150	5160
CGCCGTGGGGAGCTGCAGCTTCACGACTGGATGTCGGAGGAGTACGGGACTTGAGAG					
hrProTrpArgGluLeuGlnLeuHisAspTrpMetSerGluGluTyrrAlaAspLeuArgA					

5170 5180 5190 5200 5210 5220
 ATCCTTCTGAAGCTCTCTGGCTTCCCCTGCTCTTGACTTTCTCCACCATCTCCGGG
 spPropheLeuLysLeuSerGlyPheProCysSerTrpThrPhePheHisHisLeuArgG
 5230 5240 5250 5260 5270 5280
 AACAGATCCGCAGAGATTACCCCTGCACGACCACTTCGGGAAGCGCGCAGAGTGTGC
 luGlnIleArgArgGluPheThrLeuHisAspHisLeuArgGluGluAlaGlnSerValL
 5290 5300 5310 5320 5330 5340
 TGGGTACGCTCCGCCCTGGCGCCGACAGGGGACCGCCCGCACCTTTGTCTGGCGTCCACG
 euGlyGlnLeuArgLeuGlyArgThrGlyAspArgProArgThrPheValGlyValHisV
 5350 5360 5370 5380 5390 5400
 TCGCGCCGTGGGGACTATCTGCAGGTTATGCCCTCAGCGCTGGAAGGTGTGTGGCGGACA
 alArgArgGlyAspTyrLeuGlnValMetProGlnArgTrpLysGlyValValGlyAsps
 5410 5420 5430 5440 5450 5460
 GCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTTCG
 erAlaTyrLeuArgGlnAlaMetAspTrpPheArgAlaArgHisGluAlaProValPheV
 5470 5480 5490 5500 5510 5520
 TGGTCACCAGCAACGGCATGGAGTGGTGTAAAGAAACATCGACACCTCCCGGCGGATG
 alValThrSerAsnGlyMetGluTrpCysLysGluAsnIleAspThrSerGlnGlyAspV
 5530 5540 5550 5560 5570 5580
 TGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACAC
 alThrPheAlaGlyAspGlyGlnGluAlaThrProTrpLysAspPheAlaLeuLeuThrG

FIG. 31

5590 5600 5610 5620 5630 5640
AGTGCAACACACATTATGACCATTTGGACCTTCTGGGCTGCCTACCTGGCTG
InCysAsnHisThrIleMetThrIleGlyThrPheGlyPheTrpAlaAlaTyrLeuAlaG
5650 5660 5670 5680 5690 5700
GCGGAGACACTGTCTACCTGGCCAACTTCACCCCTGCCAGACTCTGAGTTCCTGAAGATCT
lyGlyAspThrValTyrLeuAlaAsnPheThrLeuProAspSerGluPheLeuLysIleP
5710 5720 5730 5740 5750 5760
TTAAGCCGGAGGGCCCTTCCTGCCAGTGGTGGGCATTAATGCAGACTTGTCTCCAC
heLysProGluAlaAlaPheLeuProGluTrpValGlyLeuAsnAlaAspLeuSerProL
5770 5780 5790 5800 5810 5820
TCTGGACATTGGCTAAGCCTTGAGAGCCAGGGAGACTTTCCTGAAGTAGCCTGATCTTTCT
euTrpThrLeuAlaLysProEnd
5830 5840 5850 5860 5870 5880
AGAGCCAGCAGTACGTGGCTTCAGAGGCCCTGGCATCTTCTGGAGAAAGCTTGTGTGTTC
5890 5900 5910 5920 5930 5940
TGAAGCAAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGGGAGAGTTGGAGAGAAGGGG
5950 5960 5970 5980 5990 6000
GACGTTCTGGAAGTGTCTGAATATCTAGAACTAGCAAAACATCTTTTCCTGATGGCTG
6010 6020 6030 6040 6050 6060
GCAGGCAGTTCTAGAAGCCACAGTGCCCACTGCTCTTCCAGCCCATATCTACAGTACT
6070 6080 6090 6100 6110 6120
TCCAGATGGCTGCCCCCAGGAATGGGAACTCTCCCTCTGTCTACTCTAGAAGAGGGGT
6130 6140 6150 6160 6170 6180
TACTTCTCCCTGGGTCTCCAAAGACTGAAGGAGCATATGATTGTCTCCAGAGCAAGCAT

FIG. 3J

FIG. 3K

6190	6200	6210	6220	6230	6240
TCACCAAGTCCCCCTTCTGTGTTTCTGGAGTGATTCTAGAGGGAGACTTGTCTTAGAGAGG					
6250	6260	6270	6280	6290	6300
ACCAGGTTTGATGCCCTGTGAAGAACCTGCAGGGCCCTTATGGACAGGATGGGGTCTCTGG					
6310	6320	6330	6340	6350	6360
AAATCCAGATAACTAAGGTGAAGAAATCTTTTAGTTTTTTTTTTTTTTTGGAGACAG					
6370	6380	6390	6400	6410	6420
GGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGTGATCTTGGCTCACTGCAACTTC					
6430	6440	6450	6460	6470	6480
CGCCTCCCTGTTCAAGCGATTCTCCTGTCTCAGCCTCCTGAGTAGATGGGACTACAGGC					
6490	6500	6510	6520	6530	6540
ACAGGCCATTATGCCCTGGCTAAATTTTGTATTTTGTAGTAGAGACAGGGTTTCACCATGTT					
6550	6560	6570	6580	6590	6600
GGCCGGGATGGTCTCGATCTCCTGACCTTGTCATCCACCTGTCTTGGCCTCCCAAAGTGC					
6610	6620	6630	6640	6650	6660
TGGGATTACTGGCATGAGCCACTGTGCCCCAGCCCCGGATATTTTTTTTAAATTATTTATTT					
6670	6680	6690	6700	6710	6720
ATTTATTTATTTAGACGGAGTCTTGCTCTGTAGCCCCAGGCCAGAGTGCAGTGGCGC					
6730	6740	6750	6760	6770	6780
GATCTCAGCTCACTGCAAGCTCTGCCCTCCCGGTTTCATGCCATTCTGTGCCTCAGCCTCCTG					
6790	6800	6810	6820	6830	6840
AGTAGCTGGACTACAGGGCCCCGCCACCACGCCCGGCTAAATTTTTTTTGTATTTTAGT					

FIG. 3L

6850 6860 6870 6880 6890 6900
 AGAGACGGGGTTTCATCGTGTAAACCAGGATGGTCTCGATCTCCTGACCTCGTGATCTGC
 6910 6920 6930 6940 6950 6960
 CCACCTCGGCCTCCACAGTGTCTGGGATTACCGGCGTGAGCCACCATGCCTGGCCCGGAT
 6970 6980 6990 7000 7010 7020
 AATTTTTTTTAATTTTGTAGAGACGAGGTCTTGTGATATTGCCCAGGCTGTTCTTCAAC
 7030 7040 7050 7060 7070 7080
 TCCTGGGCTCAAGCAGTCCTCCACCTTGGCCTCCAGAAATGCTGGGTTTATAGATGTGA
 7090 7100 7110 7120 7130 7140
 GCCAGCACACCGGGCCAAGTGAAGAATCTAATGAATGTGCAACCTAATTGTAGCATCTAA
 7150 7160 7170 7180 7190 7200
 TGAATGTTCCACCATTGCTGGAAAAATTGAGATGGAAAAACCAACCATCTCTAGTTGGCCA
 7210 7220 7230 7240 7250 7260
 GCGTCTTGCTCTGTTACAGTCTCTGGAAAAGCTGGGGTAGTTGGTGAGCAGAGCGGGAC
 7270 7280 7290 7300 7310 7320
 TGTGTCCAACAAGCCCCACAGCCCCCTCAAAGACTTTTTTTTGTGTTTGTGAGCAGACAG
 7330 7340 7350 7360 7370 7380
 GCTAAATGTGAACGTGGGTGAGGATCACTGCCAAAATGGTACAGCTTCTGGAGCAGA
 7390 7400 7410 7420 7430 7440
 ACTTTCCAGGGATCCAGGGACACTTTTTTTTAAAGCTCATAACTGCCAAGAGCTCCATA
 7450 7460 7470 7480 7490 7500
 TATTGGGTGAGTTCAGGTGCGCTCTCACAAATGAAGGAAGTTGGTCTTTGTCTGCAGGT

FIG. 3N

8170
TCGGCCCACTGCAA

FIG. 3N

10	*	20	*	30	*	40	*	50	*	60	*
CTGCA	GAGAG	CGCCA	CCCGG	AAGCC	ACTTT	TATAG	AAGCT	TTTAC	ACACA	ATGCT	TGATT
70	*	80	*	90	*	100	*	110	*	120	*
TTTTT	TTTTT	TTTTC	CGAGA	CGGAG	TCCTCG	CTTTG	TCGCC	CAGGC	TGGAG	TGCAG	TGGCG
130	*	140	*	150	*	160	*	170	*	180	*
CGATC	TGGGC	TCACT	GCAAG	CTCCG	CCTCC	TGGGT	TGACG	CCATT	CTCCT	GCCTC	AGCTT
190	*	200	*	210	*	220	*	230	*	240	*
CCCCA	GTAGC	TGGGA	CTACA	GGCGC	CCGCC	ACCAA	GCCTG	GCTAA	TTTTT	TTTTA	TTTTT
250	*	260	*	270	*	280	*	290	*	300	*
AGTGG	AGACA	GAGTT	TCACC	GTGTT	AGCCA	GGATG	GTCTC	GATCT	CCTGA	CCTCG	GGATC
310	*	320	*	330	*	340	*	350	*	360	*
CGCCC	GCCTC	GGCCT	CCCAA	AGTGC	TGGGA	GTATA	GGCGT	GAGCC	ACCGC	GCCTG	GCCTA
370	*	380	*	390	*	400	*	410	*	420	*
TACTT	GATTT	TTAAT	GAAAA	CATTC	TTAAA	TTTAT	ATGGC	TAACG	CAAAAT	TTATT	TTCTG
430	*	440	*	450	*	460	*	470	*	480	*
TAGGC	ATAAC	ATCAA	AAACA	CCTGG	CAGGA	CTGCC	CCATT	CCCAG	CACCTG	TCTAG	TTCTC

FIG. 4A

SEQUENCE SHEET

490	*	500	*	510	*	520	*	530	*	540	*
CCCTA	GTATC	AGTGG	GACTC	CACTG	ATGCA	CAGCT	GTGAT	CTACT	AAAAC	TTCTC	TCAAA
550	*	560	*	570	*	580	*	590	*	600	*
ACTTT	CTCCT	TAGGT	CAGCA	GCCCC	GGCCC	TGATC	TATTT	GGAAA	TCCCC	TGAAT	
610	*	620	*	630	*	640	*	650	*	660	*
AAAAG	TTGAA	TATCA	TAAAC	CAAAG	CGAAC	ACCCA	GAAAT	TCAAA	TTCAA	CCCCG	AGGTA
670	*	680	*	690	*	700	*	710	*	720	*
AAAAA	TTTCT	CAAGT	GACTG	TAGAC	GTAGA	TGTCT	CCAGT	GTCGC	CTAAT	AAGGT	AGAAG
730	*	740	*	750	*	760	*	770	*	780	*
AGGCC	AGTGC	GATAC	TGTCT	TTACA	CCCTT	AACCT	GGGTG	CTAGA	ATATT	TATCT	TCGTC
790	*	800	*	810	*	820	*	830	*	840	*
ATCAT	TTTAT	CATCC	AAACT	ATTTT	GCATA	ACTTT	CATGG	GTGCA	GAAAA	TGTTT	TTTAA
850	*	860	*	870	*	880	*	890	*	900	*
GTGCT	TGGTA	AAATT	AATAG	TGATA	TTCAT	TCATT	CATCT	CACTG	AACAG	GCAAT	AAATT
910	*	920	*	930	*	940	*	950	*	960	*
CCTTG	ACGAC	AAGGG	CCTTG	GGGGG	GGCCA	CATCT	TCATC	TTTGG	TTTAT	GAGTC	CTGTG

FIG. 4B

970	980	990	1000	1010	1020
* CGTCT TGGTA CAAGC AATAC TACTA TGAGC CGGCA AGTCA GACTT ATTTG GTAGG GGACC	* 1040	* 1050	* 1060	* 1070	* 1080
1030	1040	1050	1060	1070	1080
* AAAGG AAAGA ACATG TTTTG ATTGC TAAGA AAACA TTTTG TTCTC TATTC TTTAC TGGGC	* 1100	* 1110	* 1120	* 1130	* 1140
1090	1100	1110	1120	1130	1140
* TGGCA GGCAA AGGAA ATGTT CTTAT GAGCA CTCAC ATTGA AAACCT TAAGT TCTTC ACCAA	* 1160	* 1170	* 1180	* 1190	* 1200
1150	1160	1170	1180	1190	1200
* ATGCA GAGAC TCTGA AGGCC ACGCC GCTGC GGGCT GCCTC CACAA TTCGA CCGTC TCGGC	* 1220	* 1230	* 1240	* 1250	* 1260
1210	1220	1230	1240	1250	1260
* GGGCC ACGAG ATCCT GGCCA CGGAT GCGGT GGCCG CGCCT CTGCT CGCAC GTTCC CCCGG	* 1280	* 1290	* 1300	* 1310	* 1320
1270	1280	1290	1300	1310	1320
* CCTCT GGACT CCCTC CCTCC CTCAA TCCCT CCCTC CGGCG GCGGT CGCTG GCGGG TGGCT	* 1340	* 1350	* 1360	* 1370	* 1380
1330	1340	1350	1360	1370	1380
* AGGCC CAACG GCAGG AAGCC GACGC TATCC TCCGT TCCGC GCGGC CCGGT CCGCC TTCCG	* 1400	* 1410	* 1420	* 1430	* 1440
1390	1400	1410	1420	1430	1440
* TCTGT TCTAG GGCCT GCTCC TGCGC GGCAG CTGCT TTAGA AGGTC TCGAG CCTCC TGTAC					

FIG. 4C

SEQUENCE 348860

1450 *	1460 *	1470 *	1480 *	1490 *	1500 *
CTTCC CAGGG ATGAA CCGGG CCTTC CCTCT GGAAG GCGAG GGTTC GGGCC ACAGT GAGCG					
1510 *	1520 *	1530 *	1540 *	1550 *	1560 *
AGGGC CAGGG CCGTG GCGGC GCGCA GAGGG AAACC GGATC AGTTG AGAGA GAATC AAGAG					
1570 *	1580 *	1590 *	1600 *	1610 *	1620 *
TAGCG GATGA GCGC TTGTG GGGCG CGGCC CGGAA GCCCT CCGGC GCGGC CTGGG AGAAG					
1630 *	1640 *	1650 *	1660 *	1670 *	1680 *
GAGTG GCGCG AGGCG CCGCA GGAGG CTCCC CGGGC CTGGT CCGGC CCGCT GGGCC CCGGG					
1690 *	1700 *	1710 *	1720 *	1730 *	1740 *
CGCAG TGGAA GAAAG GGACG GGCGG TGCCC GGTG GCGGT CCTGG CCAGC TCACC TTGCC					
1750 *	1760 *	1770 *	1780 *	1790 *	1800 *
CTGGC GGCTC GCCCC GCCCG GCACT TGGGA GGAGC AGGGC CCGCG GCCTT TGCAT					
1810 *	1820 *	1830 *	1840 *	1850 *	1860 *
TCTGG GACCG CCCCC TTCCA TTCCC GGGCC AGCGG CGAGC GGCAG GCTGG AGCCG					
1870 *	1880 *	1890 *	1900 *	1910 *	1920 *
CAGCT ACAGC ATGAG AGCCG GTGCC GCTCC TCCAC GCCTG CCGAC GCGTG GCGAG CCGAG					

FIG.4D

1930	1940	1950	1960	1970
GCAGC GCTGC CTGTT CGCGC C	ATG GGG GCA CCG TGG GGC TCG CCG ACG GCG GCG	Met Gly Ala Pro Trp Gly Ser Pro Thr Ala Ala		
1980	1990	2000	2010	2020
GCG GGC GGG CGG CGC GGC TGG CGC CGA GGC GGG CTG CCA TGG ACC GTC TGT	Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Trp Thr Val Cys			
2030	2040	2050	2060	2070
GTG CTG GCG GCC GCG GGC TGT ACG TGT ACG GCG CTG ATC ACC TAC GCT TGC TGG	Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp			
2090	2100	2110	2120	2130
GGG CAG CTG CCG CCG GAG CTG CCC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC	Gly Gln Leu Pro Pro Leu Pro Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly			
2140	2150	2160	2170	2180
CTG CTG CTG TGG TGG GAG GAG CCC TTC GGG GGC CGC GAT AGC GCC CCG AGG CCG CCC	Val Leu Leu Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro			
2200	2210	2220	2230	2240
CCT GAC TGC CCG CTG CGC TGC AAC ATC AGC GGC TGC CGC CTG CTC ACC GAC CGC	Pro Asp Cys Pro Leu Arg Phe Asn Ile Ser Gly Cys Arg Leu Leu Thr Asp Arg			
2250	2260	2270	2280	2290
GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CAC CGC GAC CTC GTG AAG	Ala Ser Tyr Gly Glu Ala Aln Ala Val Leu Phe His His CAC His Arg Asp Leu Val Lys			

FIG. 4E

FIG. 4F

2300 *	2310 *	2320 *	2330 *	2340 *	2350 *
GGG CCC CCC GAC TGG CCC CCG CCC TGG GGC ATC CAG GCG CAC ACT GCC GAG GAG	Gly Pro Pro Asp Trp Pro Pro Pro Trp Gly Ile Gln Ala His Thr Ala Glu Glu				
2360 *	2370 *	2380 *	2390 *	2400 *	
GTG GAT CTG CGC GTG TTG GAC TAC GAG GAG GCA GCG GCG GCG GAA GCC CTG	Val Asp Leu Arg Val Leu Asp Tyr Glu Ala Ala Ala Ala Glu Ala Leu				
2410 *	2420 *	2430 *	2440 *	2450 *	2460 *
GGG ACC TCC AGC CCC AGG CCC CCG GGC CAG CGC TGG GTT TGG ATG AAC TTC GAG	Ala Thr Ser Ser Pro Arg Pro Pro Gly Gln Arg Trp Val Trp Met Asn Phe Gln				
2470 *	2480 *	2490 *	2500 *	2510 *	
TCG CCC TCG CAC TCC CCG GGC GAC TCG GAC TCG TTT GTG CCT TAT GGC TAC CTC TAC	Ser Pro Ser His ser Pro Gly Leu Arg Ser Leu Ala Ser Asn Leu Phe Asn Trp				
2520 *	2530 *	2540 *	2550 *	2560 *	
ACG CTC TCC TAC CCG GCG GAC TCG GAC GAC TTT GTG CCT TAT GGC TAC CTC TAC	Thr Leu Ser Tyr Arg Ala Asp Ser Asp Val Phe Val Pro Tyr Gly Tyr Leu Tyr				
2570 *	2580 *	2590 *	2600 *	2610 *	2620 *
CCC AGA AGC CAC CCC GGC GAC CCG CCC TCA GGC CTG GCC CCG CCA CTG TCC AGG	Pro Arg Ser His Pro Gly Asp Pro Pro Ser Gly Leu Ala Pro Pro Leu Ser Arg				
2630 *	2640 *	2650 *	2660 *	2670 *	
AAA CAG GGC CTG GTG GCA TGG GTG GTG AGC CAC TGG GAC GAG CGC CAG GCC CGG	Lys Gln Gly Leu Val Ala Trp Val Ser His Trp Asp Glu Arg Gln Ala Arg				

2680 * 2690 * 2700 * 2710 * 2720 * 2730 *

GTC CGC TAC TAC CAC CAA CTG AGC CAA CAT GTG ACC GTG GAC GTG TTC GGC CGG
Val Arg Tyr Tyr His Gln Leu Ser Gln His Val Thr Val Asp Val Phe Gly Arg

2740 * 2750 * 2760 * 2770 * 2780 *

CGC GGC CCC GGC CAG CCG GTG CCC GAA ATT GGG CTC CTG CAC ACA GTG GCC CGC
Gly Gly Pro Gly Gln Pro Val Pro Gln Ile Gly Leu Leu His Thr Val Ala Arg

2790 * 2800 * 2810 * 2820 * 2830 *

TAC AAG TTC TAC CTG GCT TTC GAG AAC TCG CAG CAC CTG GAT TAT ATC ACC GAG
Tyr Lys Phe Tyr Leu Ala Phe Gln Phe Glu Asn Ser Gln His Leu Asp Tyr Ile Thr Glu

2840 * 2850 * 2860 * 2870 * 2880 * 2890 *

AAG CTC TGG CGC AAC GCG TTG CTC GCT GGT GCG GCG GTG CCG GTG GTG CTG GGC CCA
Lys Leu Trp Arg Asn Ala Leu Leu Ala Gly Ala Val Pro Val Val Leu Gly Pro

2900 * 2910 * 2920 * 2930 * 2940 *

GAC CGT GCC AAC TAC GAG CCG TTT GTG CCC CGC GCG GCG GCC TTC ATC CAC GTG GAC
Asp Arg Ala Asn Tyr Glu Arg Phe Val Pro Arg Gly Ala Phe Ile His Val Asp

2950 * 2960 * 2970 * 2980 * 2990 * 3000 *

GAC TTC CCA AGT GCC TCC TCC CTG GCC TCG TAC CTG CTT TTC CTC GAC CGC AAC
Asp Phe Pro Ser Ala Ser Ser Ser Leu Ala Ser Tyr Tyr Leu Phe Leu Asp Arg Asn

3010 * 3020 * 3030 * 3040 * 3050 *

CCC GCG GTC TAT CGC CGC TAC TTC CAC TGG CGC CGG AGC TAC GCT GTC CAC ATC
Pro Ala Val Tyr Arg Arg Tyr Phe His Trp Arg Arg Ser Tyr Ala Val His Ile

FIG. 46

3060	3070	3080	3090	3100
ACC TCC TTC TGG GAC GAG CCT TGG TGC CGG GTG TGC CAG GCT GTA CAG AGG GCT				
Thr Ser Phe Trp Asp Glu Pro Trp Cys Arg Val Cys Gln Ala Val Gln Arg Ala				
3110	3120	3130	3140	3150
GGG GAC CGG CCC AAG AGC ATA CGG AAC TTG GCC AGC TGG TTC GAG CGG TGA A				
Gly Asp Arg Pro Lys Ser Ile Arg Asn Leu Ala Ser Trp Phe Glu Arg ***				
3170	3180	3190	3200	3210
GCCGC GCTCC CCTGG AAGCG ACCCA GGGGA GGCCA AGTGT TCAGC TTTT GATCC TCTAC				
3230	3240	3250	3260	3270
TGTGC ATCTC CTTGA CGGCC GCATC ATGGG AGTAA GTTCT TCAAA CACCC ATTTT TGCTC				
3290	3300	3310	3320	3330
TATGG GAAAA AAACG ATTTA CCAAT TAATA TTACT CAGCA CAGAG ATGGG GGCCC GGTTT				
3350	3360	3370	3380	3390
CCATA TTTT TGCAC AGCTA GCAAT TGGGC TCCCT TTGCT TGGGC ATCAT TGTTT				
3410	3420	3430	3440	3450
AGGGG TGAAG GAGGG GTTTC TTCCT CACCT TGTA CCAGT GCAGA AATGA AATAG CTTAG				
3470	3480	3490	3500	3510
CGGCA AGAAG CCGTT GAGGC GGTTT CCTGA ATTTC CCCAT CTGCC ACAGG CCATA TTGT				

FIG. 4H

3530	3540	3550	3560	3570	3580
* GTGCA	* CAAAT	* ACACA	* TCCCG	* ATTCA	* TTCTG
GGCCC	GCTTC	CTCAT	ACTGT	CGTTT	GACCA
3590	3600	3610	3620	3630	3640
* AAGCA	* GTGGT	* TGTAG	* AAGGA	* GCCTT	* GTTGG
AGGTG	AATT	GTGGT	TGTAG	AAGGA	CTGTG
GCTGC	AG				

FIG. 4I

pFT-3 DNA	ATGGGGCACCCTGGGGCTCGCCGACGGCGGGCGGGCGGGCGGGCGGGTG
pFT-3 AA	1 M G A P W G S P T A A A G G R R G W18
Lewis AA	1 M D . P L G . . . A A K P Q W P W13
pFT-3 DNA	GCGCCGAGCGGGGGCTGCCATGACCGTCTGTGTGCTGGGGCC-----
pFT-3 AA	19 R R G R G L P W T V C V L A A . . 33
Lewis AA	14 R R C . L A A L L 22
pFT-3 DNA	--GCCCGGCTTGACGTGTACGGCGGATCACCTAC-----GCT
pFT-3 AA	34. A G L T C T A L I T Y . . A 45
Lewis AA	23F Q L L V A V C F F S Y L R V 36
pFT-3 DNA	TGCTGGGGCAGCTGCCGCGCTGCCCTGGGCG-----TCGCCA-----
pFT-3 AA	46 C W G Q L P P L P W A . . . S P . .58
Lewis AA	37 S R D D A T G S P R A P S G S S R Q54
pFT-3 DNA	-----ACCCCGTCGCGACCG---GTGGCGGTGCTGTGTGG---TGGGAGC
pFT-3 AA	59 . . T P S R P . V G V L L W . W E 71
Lewis AA	55 D T T P T R P T L L I L L W T W . 70
pFT-3 DNA	CCTTCGGGGGGCGGATAGCGCCCCGAGCGCCCCCTGACTGC
pFT-3 AA	72P F G G R D S A P R P P P D C 86
Lewis AA	71P F H I P V A L S R C . . S 82

FIG. 5A

pFT-3 DNA	CCGCTGGGCTTCAACATCAGCGGCTGCCGCTGCTCACCGACCGCGCTCCTA	
pFT-3 AA	87 P L R F N I S G C R L L T D R A S Y104	
Lewis AA	83 E M V P G T A D C H I T A D R K V Y100	
pFT-3 DNA	CGGAGAGGCTCAGGCCGCTTTTCCACCACCGCGACCTCGTGAAGGGCCCC	
pFT-3 AA	105 G E A Q A V L F H H R D L V K G P 121	
Lewis AA	101 P Q A D T V I V H H W D I M S N P 117	
pFT-3 DNA	CCGACTGGCCCCCGCCCTGGGGCATCCAGGCGCACACTGCCGAG	
pFT-3 AA	122P D W P P P P W G I Q A H T A E 136	
Lewis AA	118K S R L P P 123	
pFT-3 DNA	GAGGTGGATCTGCGCGTGTGGACTACGAGGAGGCGAGCGGCGGCGAGAAGC	
pFT-3 AA	137 E V D L R V L D Y E E A A A A E A154	
Lewis AA	124 124	
pFT-3 DNA	CCTGGCGACCTCCAGCCCCAGCCCCCGGCCAGCGCTGGGTTGGATGAAC	
pFT-3 AA	155 L A T S S P R P P P G Q R W V W M N 171	
Lewis AA	124 136	
pFT-3 DNA	TCGAGTCGCCCTCGCACTCCCCGGGGCTGCGAAGCCTGGCAAGT	
pFT-3 AA	172F E S P S H S P G L R S L A S 186	
Lewis AA	137L E P P P N C Q H L E A L D . 150	

FIG.5B

pFT-3 DNA	AACCTCTTCAACTGGACGCTCTCTTACCGGGCGGACTCGGACGCTTTGTGCC	
pFT-3 AA	187 N L F N W T L S Y R A D S D V F V P204	
Lewis AA	151 R Y F N L T M S Y R S D S D I F T P168	
pFT-3 DNA	TTATGGCTACCTTACCCAGAAAGC---CACCCGGCGACCCGCTCAGGCC	
pFT-3 AA	205 Y G Y L Y P R S . H P G D P P S G 220	
Lewis AA	169 Y G W L E P W S G Q P A H P P . 183	
pFT-3 DNA	TGGCCCCGCACTGTCCAGGAACAGGGGCTGGTGGCATGGGTG	
pFT-3 AA	221L A P P L S R K Q G L V A W V 235	
Lewis AA	184L N . . L S A K T E L V A W A 196	
pFT-3 DNA	GTGAGCCACTGGACGAGCCAGGCCGGGTCCGCTACTACCACCACTGAG	
pFT-3 AA	236 V S H W D E R Q A R V R Y Y H Q L S253	
Lewis AA	197 V S N W K P D S A R V R Y Y Q S L Q214	
pFT-3 DNA	CCAACATGTGACCGTGGACGTTCTCGGCCGGGGCGGGCGGCGCGGTGC	
pFT-3 AA	254 Q H V T V D V F G R G G P G Q P V 270	
Lewis AA	215 A H L K V D V Y G R S . . H K P L 229	
pFT-3 DNA	CCGAAATTGGCTCTCGCACACAGTGGCCCGCTACAAGTTCTAC	
pFT-3 AA	271P E I G L L L H T V A R Y K F Y 285	
Lewis AA	230P K G T M M E T L S R Y K F Y 244	

FIG.5C

pFT-3 DNA	CTGGCTTTCGAGAACTCGCAGCACCTGGATTATATACCGAGAAAGCTCTGGCG
pFT-3 AA	286 L A F E N S Q H L D Y I T E K L W R303
Lewis AA	245 L A F E N S L H P D Y I T E K L W R262
pFT-3 DNA	CAACGCGTTGCTCGCTGGGGCGGTGCCGGTGGTGGTGGCCAGACCGTGCCA
pFT-3 AA	304 N A L L A G A V P V V L G P D R A 320
Lewis AA	263 N A L E A W A V V V L G P S R S 279
pFT-3 DNA	ACTACGAGCGCTTTGTGCCCGCGCGCTTCATCCACGTGGAC
pFT-3 AA	321N Y E R F V P R G A F I H V D 335
Lewis AA	280N Y E R F L P P D A F I H V D 294
pFT-3 DNA	GACTTCCCAAGTGCCTCCTCCCTGGCCCTCGTACCTGCTTTCTCGACCGCAA
pFT-3 AA	336 D F P S A S S L A S Y L L F L D R N353
Lewis AA	295 D F Q S P K D L A R Y L Q E L D K D312
pFT-3 DNA	CCCCGCGGTCTATCGCCGCTACTTCCACTGGCGC-----CGGA
pFT-3 AA	354 P A V Y R R Y F H W R . . . R 365
Lewis AA	313 H A R Y L S Y F R W R E T L R P R 329
pFT-3 DNA	GCTACGCTGTCCACATCACCTCCTC---TGGACGAGCCTTGG
pFT-3 AA	366S Y A V H I T S F . W D E P W 379
Lewis AA	330S F S W A L D . . F 337

FIG.5D

pFT-3 DNA	TGCCGGGTGTGCCAGGCTGTACAGAGGGCTGGGGACCGGCCCAAGAGCATACG	
pFT-3 AA	380 C R V C Q A V Q R A G D R P K S I R397	:
Lewis AA	338 C K A C W K L Q Q E S . R Y Q T V R354	:
pFT-3 DNA	GAACTTGGCCAGCTGGTTCGAGCGGTGA	
pFT-3 AA	398 N L A S W F E R 405	:
Lewis AA	355 S I A A W F T . 361	:

FIG.5E

0956423 360601

Sequence VI

-120 TTTATGACAGCTGTGTCAATAATTATAACAGCTTCTCTCAGGACACTGTGGCCAGGAAG

-60 TGGTGATCTTCTTAATGACCCCTCACTCCTCTCTCCTCTCTTCCCAGCTACTCTGACCC

1 M D P L G P A K P Q W L W R R C L A G L
 ATGGATCCCTGGGCCAGCCAGCCAGTGGCTGTGGCCCGCTGTCTGGCCGGCTG
 ATGGATCCCTGGGTGCAGCCAGCCACAATGGCCATGGCCCGCTGTCTGGCCGCACTG

61 L F Q L L V A V C F F S Y L R V S R D D
CTGTT CAGCTGCTGGTGGCTGTGTGTTTCTTCTCTACCTGCGTGTCGCCGAGACGAT
CTATTT CAGCTGCTGGTGGCTGTGTGTTTCTTCTCTACCTGCGTGTCGCCGAGACGAT

121 A T G S P R P G L M A V E P V T G A P N
GCCACTGGATCCCCCTAGGCCAGGCTTATGGCAGTGGAACTGTACCGGGCTCCCAAT
GCCACTGGATCCCCCTAGG-----GCTCCCACTG

181 G S R C Q D S M A T P A H P T L L I L L
GGTCCCGCTGCCAGACAGCATGGCGACCCCTGCCACCCACCCACTGATCCTGCTG
GGTCCCTCCGACAGGACACC-----ACTCCACCGGCCACCCCTCCTGATCCTGCTA
S R T R

FIG. 6A

W T W P F N T P V A L P R C S E M V P G
 241 TGGACGTGGCCTTTTAAACACACCCGTGGTCTGCCCCGCTGCTCAGAGATGGTGCCCCGGC
 TGGACATGGCCTTTCCACATCCCTGTGGTCTGTGCCCGCTGTTTCAGAGATGGTGCCCCGGC
 H I S

A A D C N I T A D S S V Y P Q A D A V I
 301 GCGCCGACTGCAACATCACTGCCGACTCCAGTGTGTACCCACAGGACGCGGTCAATC
 ACAGCCGACTGCCACATCACTGCCGACCGCAAGGTGTACCCACAGGACGACACGGTCAATC
 T H K T

V H H W D I M Y N P S A N L P P P T R P
 361 GTGCACCACTGGGATATCATGTACAACCCAGTGCCAACTCCCGCCCCCACCAGGCCG
 GTGCACCACTGGGATATCATGTCCAACCCCTAAGTCACGCTCCCACTTCCCCGAGGCCG
 S K S R S P

Q G Q R W I W F S M E S P S N C R H L E
 421 CAGGGCAGCGCTGGATCTGGTTTCAGCATGGAGTCCCCCAGCAACTGCCGGCACCTGGAA
 CAGGGCAGCGCTGGATCTGGTTCAACTTGGAGCCACCCCTAACTGCCAGCACCTGGAA
 N L P P Q

A L D G Y F N L T M S Y R S D S D I F T
 481 GCCCTGGACGGATACTTCAATCTCACCATGTCTACCGCAGGACTCCGACATCTTCACG
 GCCCTGGACAGATACTTCAATCTCACCATGTCTACCGCAGGACTCCGACATCTTCACG
 R

P Y G W L E P W S G Q P A H P P L N L S
 541 CCCTACGGCTGGAGCCGCTGGTCCGGCCAGCCTGCCACCCACCGCTCAACCTCTCG
 CCCTACGGCTGGAGCCGCTGGTCCGGCCAGCCTGCCACCCACCGCTCAACCTCTCG

FIG. 6B

601 A K T E L V A W A V S N W K P D S A R V
 GCCAAGACOGAGCTGGTGGCCCTGGCGGTGTCCAACTGGAAGCCGGACTCGGCCAGGGTG
 GCCAAGACOGAGCTGGTGGCCCTGGCGGTGTCCAACTGGAAGCCGGACTCGGCCAGGGTG

661 R Y Y Q S L Q A H L K V D V Y G R S H K
 CGCTACTACGAGCCTGCAGGCTCATCTCAAGGTGGACGTGTACGGACGCTCCACAAG
 CGCTACTACGAGCCTGCAGGCTCATCTCAAGGTGGACGTGTACGGACGCTCCACAAG

721 P L P K G T M M E T L S R Y K F Y L A F
 CCCCTGCCCCAAGGGACCATGATGGAGACGCTGTCCGGTACAAGTTCTATCTGGCCTTC
 CCCCTGCCCCAAGGGACCATGATGGAGACGCTGTCCGGTACAAGTTCTATCTGGCCTTC

781 E N S L H P D Y I T E K L W R N A L E A
 GAGAACTCCTTGACCCCGACTACATCACCGAAGCTGTGGAGGAACGCCCTGGAGGCC
 GAGAACTCCTTGACCCCGACTACATCACCGAAGCTGTGGAGGAACGCCCTGGAGGCC

841 W A V P V V L G P S R S N Y E R F L P P
 TGGGCCGTGCCCGTGGTGGTGGCCCGCAGCAGAAGCAACTACGAGAGGTTCTTCCCGCCC
 TGGGCCGTGCCCGTGGTGGTGGCCCGCAGCAGAAGCAACTACGAGAGGTTCTTCCCGCCC

901 D A F I H V D D F Q S P K D L A R Y L Q
 GACGCCTTCATCCACGTGGATGACTTCCAGAGCCCCAAGGACCTGGCCCCGTACCTGCAG
 GACGCCTTCATCCACGTGGACGACTTCCAGAGCCCCAAGGACCTGGCCCCGTACCTGCAG

961 E L D K D H A R Y L S Y F R W R E T L R
 GAGCTGGACAAGGACCAAGCCCGCTACCTGAGCTACTTTCGCTGGCGGAGACGCTGCGG
 GAGCTGGACAAGGACCAAGCCCGCTACCTGAGCTACTTTCGCTGGCGGAGACGCTGCGG

FIG. 6C

P R S F S W A L A F C K A C W K L Q Q E
1021 CCTCGCTCCTTCAGCTGGGCACTGGCTTCTGCAAGGCCTGCTGGAAGCTGCAGCAGGAA
CCTCGCTCCTTCAGCTGGGCACTGGATTCTGCAAGGCCTGCTGGAACCTGCAGCAGGAA
D

S R Y Q T V R S I A A W F T U
1081 TCCAGGTACCAGACGGTGCGCAGCATAGCGGCTTGTTTACCTGAGAGGCCGCGCATGGGG
TCCAGGTACCAGACGGTGCGCAGCATAGCGGCTTGTTTACCTGA

1141 CCTGGGCTGCCAGGGACCTCACTTCCCAGGGCCTCACCTACCTAGGGTC // TCTAGA

FIG. 6D

$\alpha(1,3)$ FT DNA (-128)	TTTTCTCA
$\alpha(1,3)$ FT DNA (-120)	TCTGTGAACAGGAATAATAACAGCTCTTCTCAGGACTCATGGCCTGGAGCTTTGGTAAG
$\alpha(1,3)$ FT DNA (-60)	CAGGAGATTGTCATCAATGACCCCTCACTCCTCTCTCTCCCACTTCCAGAGACTCTGACCCC
$\alpha(1,3)$ FT AA	M D P L G P A K P Q W S W R C C L T T L
$\alpha(1,3)$ DNA (1)	ATGGATCCCCCTGGGCCCCGCAAGCCACAGTGGTGGTGGCGCTGCTGTCTGACCACGCTG
Lewis FT DNA	 ATGGATCCCCCTGGGTGCAGCCCAAGCCACAATGGCCATGGCGCGCTGTCTGGCGCACTG
$\alpha(1,3)$ FT AA	L F Q L L M A V C F F S Y L R V S Q D D
$\alpha(1,3)$ FT DNA (61)	CTGTTTCAGCTGCTGATGGCTGTGTGTTTCTTCTCCTATCTGCGTGTGTCTCAAGACGAT
	 CTATTTCAGCTGCTGGTGGCTGTGTGTTTCTTCTCCTACCTGCGTGTGTCTCCGAGACGAT
$\alpha(1,3)$ FT AA	P T V Y P N G S R F P D S T G T P A H S
$\alpha(1,3)$ FT DNA (121)	CCCACTGTGTACCCCTAATGGGTCC...CGCTTCCCA..GACAGCACAGGACCCCGCCCACTCC
Lewis FT DNA	 GCCACTGGATCCCCCTAG.GGCTCCCAGTGGGTCTCTCCGACAGGACACC.ACTCCCACCCGCCCC
$\alpha(1,3)$ FT AA	I P L I L L W T W P F N K P I A L P R C
$\alpha(1,3)$ FT DNA (181)	ATCCCCCTGATCCTGCTGTGGACGTGGCCCTTTTAACAAACCCATAGCTCTGCCCGCTGC
Lewis FT DNA	 ACCTCCTGATCCTGCTATGGACATGGCCCTTTCCACATCCCTGTGGCTCTGTCCCGCTGT

FIG. 7A

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (241)
 Lewis FT DNA

S E M V P G T A D C N I T A D R K V Y P
 TCAGAGATGGTGCCTGGCAGCGCTGACTGCAACATCACTGCCGACCGCAAGGTGTATCCA
 |||||
 TCAGAGATGGTGCCTGGCAGCGCTGACTGCCACATCACTGCCGACCGCAAGGTGTATCCA

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (301)
 Lewis FT DNA

Q A D A V I V H H R E V M Y N P S A Q L
 CAGGCAGACGCGGTCACTCGTGACACCGAGAGGTGATGTACAACCCAGTGCCAGCTC
 |||||
 CAGGCAGACACGCGGTCACTCGTGACCACTGGGATATCATGTCCAACCTAAGTCACGCCTC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (361)
 Lewis FT DNA

P R S P R R Q G Q R W I W F S M E S P S
 CCACGCTCCCCGAGGCGGAGGCGATGATCTGTTTCAGCATGGAGTCCCCAAGC
 |||||
 CCACCTTCCCCGAGGCGGAGGCGGCTGGATCTGTTCAACTTGGAGCCACCCCT

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (421)
 Lewis FT DNA

H C W Q L K A M D G Y F N L T M S Y R S
 CACTGCTGGCAGCTGAAGCCATGGACGGATACTTCAATCTCACCATGTCTACCGCAGC
 |||||
 AACTGCCAGCACCTGGAAGCCCTGGACAGATACTTCAATCTCACCATGTCTACCGCAGC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (481)
 Lewis FT DNA

D S D I F T P Y G W L E P W S G Q P A H
 GACTCCGACATCTTACGCCCTACGGCTGGCTGGAGCCGTTGTCGGCCAGCCTGCCAC
 |||||
 GACTCCGACATCTTACGCCCTACGGCTGGCTGGAGCCGTTGTCGGCCAGCCTGCCAC

FIG. 7B

$\alpha(1,3)$ FT AA	P P L N L S A K T E L V A W A V S N W G
$\alpha(1,3)$ FT DNA (541)	CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCTGGCAGTGTCCAACCTGGGGG CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCTGGCAGTGTCCAACCTGGAAG
Lewis FT DNA	

	P	N	S	A	R	V	R	Y	Q	S	L	Q	A	H	L	K	V	D	V
$\alpha(1,3)$ FT AA	C	C	A	A	T	C	G	G	T	G	C	T	A	C	C	A	G	G	T
$\alpha(1,3)$ FT DNA (601)	C	C	A	A	T	C	G	G	T	G	C	T	A	C	C	A	G	G	T
Lewis FT DNA	C	C	G	G	A	T	C	G	G	T	G	C	T	A	C	C	A	G	G
	C	C	G	G	A	T	C	G	G	T	G	C	T	A	C	C	A	G	G
	C	C	G	G	A	T	C	G	G	T	G	C	T	A	C	C	A	G	G

$\alpha(1,3)$ FT AA	Y G R S H K P L P Q G T M E T L S R Y
$\alpha(1,3)$ FT DNA (661)	TACGGACGCTCCACAAGCCCTGCCCCAGGAACCATGATGGAGACGCTGTCCCGTAC TACGGACGCTCCACAAGCCCTGCCCAAGGGACCATGATGGAGACGCTGTCCCGTAC
Lewis FT DNA	

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (721)
 ...
 Lewis FT DNA

$\alpha(1,3)$ FT AA	R N A L E A W A V P V L G P S R S N Y
$\alpha(1,3)$ FT DNA (781)	AGGAACGCCCTGGAGGCTGGGCCGTGCCCGTGGTCTGGGCCCCAGCAGAAAGCAACTAC
	AGGAACGCCCTGGAGGCTGGGCCGTGCCCGTGGTCTGGGCCCCAGCAGAAAGCAACTAC
Lewis FT DNA	

FIG. 7C

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (841)
 Lewis FT DNA

E R F L P P D A F I H V D D F Q S P K D
 GAGAGTTCTGCGCACCCGACGCTTTCATCCAGTGGACGACTTCCAGAGCCCCAAGGAC
 |||||
 GAGAGTTCTGCGCACCCGACGCTTTCATCCAGTGGACGACTTCCAGAGCCCCAAGGAC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (901)
 Lewis FT DNA

L A R Y L Q E L D K D H A R Y L S Y F R
 CTGGCCCGGTACTGTCAGGAGCTGGACAAGGACCAAGGACCGCCGCTACTGAGCTACTTTCGC
 |||||
 CTGGCCCGGTACTGTCAGGAGCTGGACAAGGACCAAGGACCGCCGCTACTGAGCTACTTTCGC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (961)
 Lewis FT DNA

W R E T L R P R S F S W A L A F C K A C
 TGGCGGAGACGCTGCGGCTCGCTCCTTCAGCTGGGCACTCGCTTCTGCAAGGCCTGC
 |||||
 TGGCGGAGACGCTGCGGCTCGCTCCTTCAGCTGGGCACTGGATTCTGCAAGGCCTGC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (1021)
 Lewis FT DNA

W K L Q E E S R Y Q T R G I A A W F T Stop
 TGGAAACTGCAGGAGGAATCCAGGTACCAGACACGCGGC...ATAGCGGCTTGGTTACCTGA
 |||||
 TGGAAACTGCAGGAGGAATCCAGGTACCAGACGCGGTGCGCAGCATAGCGGCTTGGTTACCTGA

GAGGCTGGTGGGCTGGGCTGCCAGGAACCTCATTTCTGGGGCTCACCTGAGTG
 GGGCCCTCATCTACCTAAGGACTCGTTTGCTGAAGCTTCACTGCTGAGGACTCACCT
 GCTGGACGGTCACTGTTGCAGCTTCACTGCTGGGATTCACCTACCTGGGTCCTC
 ACTTCTGGGCTCACCTGCTGGAGTCTTGGTGGCCAGGTATGTCCTTACCTGGGA
 TTTACATGCTGGCTTCCAGGAGCGTCCCTGCGGAAGCCTGGCTGCTGGGATGTCTC
 CTGGGACTTTCCTACTGGGACCTCGGCTGTTGGGACTTACCTGCTGGGACCTGCT
 CCCAGAGACCTTCCACACTGAATCTCACCTGCTAGGAGCCTCACCTGCTGGGACCTCAC
 CCTGGAGGCACTGGGCCCTGGGAAT

FIG. 7D

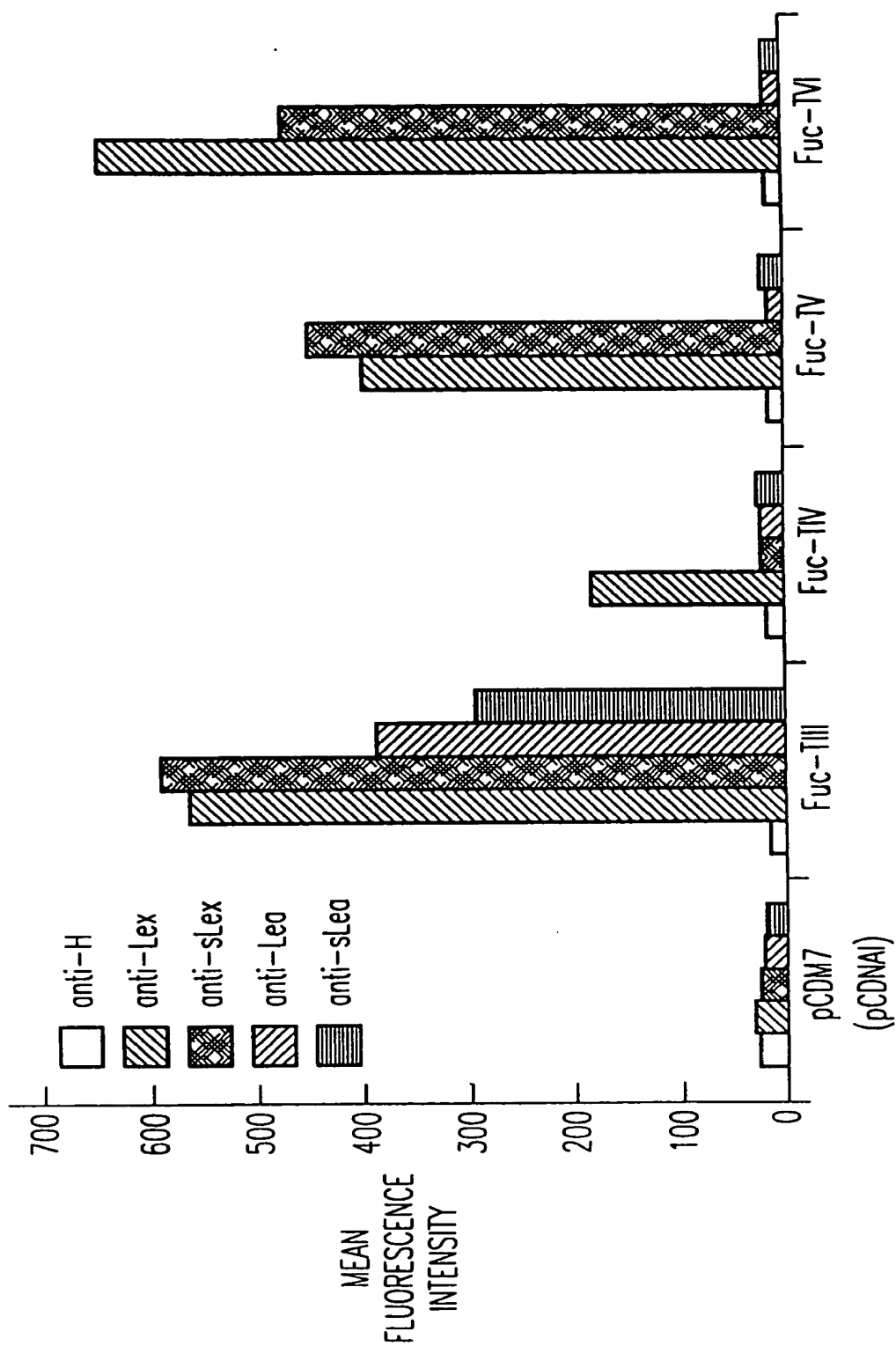


FIG. 8